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LOCUS
            AF186371
                                  3014 bp
                                            DNA
                                                   linear
                                                            BCT 10-SEP-2002
DEFINITION
            Streptomyces coelicolor A3(2) AhpD (ahpD), AhpC (ahpC), and OxyR
            (oxyR) genes, complete cds.
ACCESSION
            AF186371
VERSION
            AF186371.1 GI:6288864
SOURCE
            Streptomyces coelicolor A3(2)
  ORGANISM
           Streptomyces coelicolor A3(2)
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales:
            Streptomycineae; Streptomycetaceae; Streptomyces.
REFERENCE
               (bases 1 to 3014)
  AUTHORS
           Hahn, J.S., Oh, S.Y. and Roe, J.H.
  TITLE
           Role of OxyR as a Peroxide-Sensing Positive Regulator in
           Streptomyces coelicolor A3(2)
  JOURNAL
           J. Bacteriol. 184 (19), 5214-5222 (2002)
           22206464
  MEDLINE
   PUBMED
           12218006
REFERENCE
               (bases 1 to 3014)
  AUTHORS
           Hahn, J.-S. and Roe, J.-H.
           Role of OxyR as a regulator of the ahpCD operon encoding alkyl
  TITLE
           hydroperoxide reductase system in Streptomyces coelicolor
  JOURNAL
           Unpublished
REFERENCE
              (bases 1 to 3014)
           3
  AUTHORS
           Hahn, J.-S. and Roe, J.-H.
  TITLE
           Direct Submission
  JOURNAL
           Submitted (15-SEP-1999) Microbiology, Seoul National University,
           Kwan-Ak Gu, Shin-Lim 9Dong, San 56-1, Seoul 151-742, Korea
  Query Match
                        13.0%; Score 217.2; DB 1; Length 3014;
  Best Local Similarity
                        53.6%; Pred. No. 2.8e-43;
  Matches 478; Conservative
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                                  Mismatches 408;
                                                   Indels
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         492 TGAGCAATAAAGAGTACCGGCCCACACTCGCCCAGCTTCGCACCTTTGTCACCATCGCAG 551
Qy-
            - 11 111 111 111
                             Db
         1826 TGTCCAGTAAGAAGACAGCCCAGCCTCGCTCAGCTGCGGGCTTCCGACGCGGTCGCCG 1885
         552 AATGCAAGCACTTTGGTACTGCCACCAAGCTGTCCATTTCGCAGCCATCCCTCTCCC 611
Qу
                   111
                                                      ++++
        Db
         612 AGGCACTTGTCGCATTAGAAACAGGCCTGGGAGTTCAGCTGATTGAACGCTCCACCCGCA 671
Qу
                  11
                     111 | 111
                                     1
                                                \Pi
                                                    Db
        1946 GTGCCGTTTCCGCCCTGGAAGAGGCACTGGGTCTCACCCTCCTGGGGCGTACGACGCGCA 2005
         672 AGGTCATTGTCACCCCAGCGGGCGAGAAGTTGCTGCCATTCGCCAAATCCACCCTTGACG 731
Qу
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                                      ^{-1}
                                           1111 1
Db
        2006 AGGTGCTGTCCCCGGCCGGCGCACGGCTCGCGGTGCGGACCAAGGCGGTACTGGCGG 2065
         732 CGGCGGAGTCTTTCCTCTCCCACGCCAAGGGCGCCAACGGTTCGCTCACTGGACCGTTGA 791
Qy
                       -11111
                                1 11 111
                                          -1
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Db
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         792 CCGTAGGCATCATCCCCACGGCGGCTCCTTACATTTTGCCGTCAATGCTGTCCATCGTGG 851
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        2126 GGCTCGGCGTCATCCCGACCGTGGCGCCCTATGTGCTGCCGACGGTGCTGCGCCTCGTCC 2185
Db
         852 ATGAAGAATATCCAGATCTGGAACCTCACATCGTCGAGGACCAAACCAAGCATCTTCTCG 911
Qу
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	Db	
	Qу	1032 CCTTCGCCGGCCCAAGACTTAGAACTATCCGCCTTAGAAGACCTCGATCTGCTGCTTC 1091
	Dр	2366 GACTCGGCGGCGGGAGGCCTGGAGCCTCGGTGCTGCGCGAGCTGAAGCTGCTGCTGC 2425
	QY .	1092 TCGACGACGGACACTGCCTCCACGACCAAATTGTGGACCTGTGCCGCCGCGGAGACATCA 1151
	Db	2426 TCGACGAGGGGCACTGCCTGCGCGACCAGGCGCTCGACATCTGCCGGGAGGCGG 2479
	Qу	1152 ACCCCATTAGCTCCACTACTGCTGTCACCCGCGCATCCAGCCTTACCACCGTCATGCAGC 1211
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